

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/373,857DATE: 06/08/95
TIME: 10:52:19

INPUT SET: S4067.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

H5

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Lobb, Roy R.

(ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street, Suite 510

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/373,857

(B) FILING DATE: 18-JAN-1995

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/284,603

(B) FILING DATE: 11-AUG-1994

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/835,139

(B) FILING DATE: 12-FEB-1992

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US93/00924

(B) FILING DATE: 02-FEB-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Louis Myers (PLM)

(B) REGISTRATION NUMBER: 35,965

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47      (C) REFERENCE/DOCKET NUMBER: BGP-031USCP
48
49      (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: (617)227-7400
51          (B) TELEFAX: (617)227-5941
52
53
54      (2) INFORMATION FOR SEQ ID NO:1:
55
56          (i) SEQUENCE CHARACTERISTICS:
57              (A) LENGTH: 360 base pairs
58              (B) TYPE: nucleic acid
59              (C) STRANDEDNESS: single
60              (D) TOPOLOGY: linear
61
62          (ii) MOLECULE TYPE: cDNA
63
64
65          (ix) FEATURE:
66              (A) NAME/KEY: CDS
67              (B) LOCATION: 1..360
68
69          (ix) FEATURE:
70              (A) NAME/KEY: misc_feature
71              (B) LOCATION: 1
72              (D) OTHER INFORMATION: /note= "pBAG159 insert:
73                  HP1/2 heavy vchain variable region; amino acid 1 is
74                  Glu (E) but Gln (Q) may be substituted"
75
76
77          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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79      GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA      48
80      Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
81          1              5              10              15
82
83      GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT      96
84      Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
85          20              25              30
86
87      ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA      144
88      Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
89          35              40              45
90
91      AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG      192
92      Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
93          50              55              60
94
95      GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG      240
96      Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
97          65              70              75              80
98
99      CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA      288
  
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100 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
101 85 90 95
102
103 GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA 336
104 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
105 100 105 110
106
107 GGG ACC ACG GTC ACC GTC TCC TCA 360
108 Gly Thr Thr Val Thr Val Ser Ser
109 115 120
110
111
112 (2) INFORMATION FOR SEQ ID NO:2:
113
114 (i) SEQUENCE CHARACTERISTICS:
115 (A) LENGTH: 120 amino acids
116 (B) TYPE: amino acid
117 (D) TOPOLOGY: linear
118
119 (ii) MOLECULE TYPE: protein
120
121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
122
123 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
124 1 5 10 15
125
126 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
127 20 25 30
128
129 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
130 35 40 45
131
132 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
133 50 55 60
134
135 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
136 65 70 75 80
137
138 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
139 85 90 95
140
141 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
142 100 105 110
143
144 Gly Thr Thr Val Thr Val Ser Ser
145 115 120
146
147 (2) INFORMATION FOR SEQ ID NO:3:
148
149 (i) SEQUENCE CHARACTERISTICS:
150 (A) LENGTH: 318 base pairs
151 (B) TYPE: nucleic acid
152 (C) STRANDEDNESS: single

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153 (D) TOPOLOGY: linear

154

155 (ii) MOLECULE TYPE: cDNA

156

157

158 (ix) FEATURE:

159 (A) NAME/KEY: CDS

160 (B) LOCATION: 1..318

161 (D) OTHER INFORMATION: /product= "HP1/2 light
162 chain variable region"

163

164 (ix) FEATURE:

165 (A) NAME/KEY: misc_feature

166 (B) LOCATION: 1

167 (D) OTHER INFORMATION: /note= "pBAG172 insert:
168 HP1/2 light chain variable region"

169

170

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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173 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA 48

174 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

175 1 5 10 15

176

177 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96

178 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp

179 20 25 30

180

181 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144

182 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

183 35 40 45

184

185 TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192

186 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

187 50 55 60

188

189 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240

190 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala

191 65 70 75 80

192

193 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC 288

194 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr

195 85 90 95

196

197 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC 318

198 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile

199 100 105

200

201

202 (2) INFORMATION FOR SEQ ID NO:4:

203

204 (i) SEQUENCE CHARACTERISTICS:

205 (A) LENGTH: 106 amino acids

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206 (B) TYPE: amino acid
207 (D) TOPOLOGY: linear
208
209 (ii) MOLECULE TYPE: protein
210
211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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213 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
214 1 5 10 15
215
216 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
217 20 25 30
218
219 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
220 35 40 45
221
222 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
223 50 55 60
224
225 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
226 65 70 75 80
227
228 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
229 85 90 95
230
231 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
232 100 105
233
234
235

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/373,857

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